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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=11; day=18; hr=18; min=57; sec=29; ms=694;
]

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Reviewer Comments:

<210> 25

<211> 189

<212> DNA

<213> Synthetic intron

<400> 25

<210> 29

<211> 20

<212> PRT

<213> Synthetic

The above <213> responses for sequence id#'s 25 and 29 are both invalid, please correct the remaining sequences showing similar errors.

Application No: 10596010 Version No: 2.0

Input Set:

Output Set:

Started: 2008-10-21 11:04:20.060
Finished: 2008-10-21 11:04:21.978
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 918 ms
Total Warnings: 16
Total Errors: 2
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (26)
E 356	Organism is not permitted in <213> in SEQ ID (29)
E 356	Organism is not permitted in <213> in SEQ ID (30)

SEQUENCE LISTING

<110> Copenhagen University Tech Trans Enheden
Andreasson, Erik
Jenkins, Tom
Mundy, John
Petersen, Nikolaj H.T.
Brodersen, Peter
Thorgrimsen, Stefan
Rocher, Anne

<120> Plant Disease Resistance and SAR Regulator Protein

<130> 09663.0068USWO

<140> 10596010

<141> 2008-10-21

<150> PCT/DK2004/000822

<151> 2004-11-26

<150> DK PA200301759

<151> 2003-11-28

<150> US 60/526,319

<151> 2003-12-01

<160> 30

<170> PatentIn version 3.5

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48

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Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu
20 25 30

96

agt gtt cac aaa gac tct cac aaa atc aag aaa cct cca aaa cac cct
Ser Val His Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro
35 40 45

144

gcg ccg ccg cca aat cgt gac caa ccg ccg ccg tat att cct aga gag
Ala Pro Pro Pro Asn Arg Asp Gln Pro Pro Pro Tyr Ile Pro Arg Glu

192

50	55	60	
ccg gtg gtt atc tac gcc gta tcc ccc aag gtt gta cac gca acc gcg Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Ala Thr Ala			240
65	70	75	80
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85	90	95	
gtt ttc ctc gaa tct ggc ggc ggt gga gat gtt tca ccg gcg gcg agg Val Phe Leu Glu Ser Gly Gly Gly Asp Val Ser Pro Ala Ala Arg			336
100	105	110	
cta gcg tcc acg gaa aat gct agt cca aga gga gga aaa gaa ccg gct Leu Ala Ser Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro Ala			384
115	120	125	
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130	135	140	
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145	150	155	160
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165	170	175	
ggg atg ttt tcg ccg gct ata cca ctg gga tta ttc tcg ccg gcg gga Gly Met Phe Ser Pro Ala Ile Pro Leu Gly Leu Phe Ser Pro Ala Gly			576
180	185	190	
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35 40 45

Ala Pro Pro Pro Asn Arg Asp Gln Pro Pro Pro Tyr Ile Pro Arg Glu
50 55 60

Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Ala Thr Ala
65 70 75 80

Ser Glu Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser Gly
85 90 95

Val Phe Leu Glu Ser Gly Gly Gly Asp Val Ser Pro Ala Ala Arg
100 105 110

Leu Ala Ser Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro Ala
115 120 125

Ala Arg Asp Glu Thr Val Glu Ile Asn Thr Ala Met Glu Glu Ala Ala
130 135 140

Glu Phe Gly Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser Pro Ala Leu
145 150 155 160

Leu Pro Thr Ala Ser Thr Gly Ile Phe Ser Pro Met Tyr His Gln Gly
165 170 175

Gly Met Phe Ser Pro Ala Ile Pro Leu Gly Leu Phe Ser Pro Ala Gly
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ata cca ttg aaa gtc cgt gga gat tcg cac aag atc atc aag aag cca		96	
Ile Pro Leu Lys Val Arg Gly Asp Ser His Lys Ile Ile Lys Lys Pro			
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cca cta gcg ccg cca cac ccg caa cca caa cca caa acc cat cag		144	
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Gln Glu Pro Ser Gln Ser Arg Pro Pro Pro Gly Pro Val Ile Ile Tyr			
50	55	60	
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65	70	75	80
ttg gtc caa cgt ctc aca ggt aaa acc tcc acc tcc aca aca tcc tcc		288	
Leu Val Gln Arg Leu Thr Gly Lys Thr Ser Thr Ser Thr Ser Ser			
85	90	95	
tcc tat tct tca tct acg tca gca cca aaa gac gcg tca aca atg gtt		336	
Ser Tyr Ser Ser Thr Ser Ala Pro Lys Asp Ala Ser Thr Met Val			
100	105	110	
gat aca tct cat ggg ttg ata tct ccg gcg gct cgg ttt gct gtt aca		384	
Asp Thr Ser His Gly Leu Ile Ser Pro Ala Ala Arg Phe Ala Val Thr			
115	120	125	
gag aag gct aat atc tca aac gaa cta ggg aca ttt gtt gga ggc gaa		432	
Glu Lys Ala Asn Ile Ser Asn Glu Leu Gly Thr Phe Val Gly Gly Glu			
130	135	140	

ggg act atg gat caa tat tat cat tat cat cat cat cat cat caa Gly Thr Met Asp Gln Tyr Tyr His Tyr His His His His His Gln	145	150	155	160	480
gaa caa caa cat caa aat caa ggg ttc gag cgg cca agt ttc cac cat Glu Gln Gln His Gln Asn Gln Gly Phe Glu Arg Pro Ser Phe His His	165	170	175		528
gct ggg att tta tcg ccg gga cct aat tct ctg ccg tcg gta tca ccg Ala Gly Ile Leu Ser Pro Gly Pro Asn Ser Leu Pro Ser Val Ser Pro	180	185	190		576
gac ttc ttt tcc act att gga cca acc gat cca caa ggt ttt tcg tcg Asp Phe Phe Ser Thr Ile Gly Pro Thr Asp Pro Gln Gly Phe Ser Ser	195	200	205		624
ttc ttt aat gac ttt aac tct atc ctt cag agt agt cca tcg aag att Phe Phe Asn Asp Phe Asn Ser Ile Leu Gln Ser Ser Pro Ser Lys Ile	210	215	220		672
cag tct cct tct tct atg gac ctt ttc aac aat ttc ttt gat tct tga Gln Ser Pro Ser Ser Met Asp Leu Phe Asn Asn Phe Phe Asp Ser	225	230	235		720
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Gln Glu Pro Ser Gln Ser Arg Pro Pro Pro Gly Pro Val Ile Ile Tyr 50 55 60					
Thr Val Ser Pro Arg Ile Ile His Thr His Pro Asn Asn Phe Met Thr 65 70 75 80					
Leu Val Gln Arg Leu Thr Gly Lys Thr Ser Thr Ser Thr Ser Ser 85 90 95					
Ser Tyr Ser Ser Ser Thr Ser Ala Pro Lys Asp Ala Ser Thr Met Val					

100 105 110

Asp Thr Ser His Gly Leu Ile Ser Pro Ala Ala Arg Phe Ala Val Thr
115 120 125

Glu Lys Ala Asn Ile Ser Asn Glu Leu Gly Thr Phe Val Gly Gly Glu
130 135 140

Gly Thr Met Asp Gln Tyr Tyr His Tyr His His His His His Gln
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Ala Gly Ile Leu Ser Pro Gly Pro Asn Ser Leu Pro Ser Val Ser Pro
180 185 190

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195 200 205

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aactctttt	agaaaata	atg	gat	ccg	tcg	gag	tct	ttc	gcc	ggc	aat	171				
		Met	Asp	Pro	Ser	Glu	Ser	Phe	Ala	Gly	Gly	Asn				
		1		5					10							
cct	tcc	gac	caa	cag	aac	cag	aaa	cgt	ctt	cag	atc	tgt	ggt	cct	219	
Pro	Ser	Asp	Gln	Gln	Asn	Gln	Lys	Arg	Gln	Ile	Cys	Gly	Pro			
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cgt	ccc	tca	cct	ctc	agc	gtc	aac	aaa	gac	tct	cac	aag	atc	aag	aaa	267
Arg	Pro	Ser	Pro	Leu	Ser	Val	Asn	Lys	Asp	Ser	His	Lys	Ile	Lys	Lys	
30		35						40								
cct	cct	aaa	cac	cct	gct	cct	ccg	cct	cag	cat	cg	gac	caa	gct	ccg	315
Pro	Pro	Lys	His	Pro	Ala	Pro	Pro	Pro	Gln	His	Arg	Asp	Gln	Ala	Pro	
45		50						55								
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Leu	Tyr	Ala	Ala	Arg	Glu	Pro	Val	Val	Ile	Tyr	Ala	Val	Ser	Pro	Lys	
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gtc	gtc	cac	acc	aca	gcc	tcg	gat	ttc	atg	aac	gtc	gtc	cag	cgt	ctc	411
Val	Val	His	Thr	Ala	Ser	Asp	Phe	Met	Asn	Val	Val	Gln	Arg	Leu		
80		85			90											
acc	ggc	atc	tca	tcc	gcc	gtc	ttc	ctc	gaa	tcc	ggt	aac	ggc	gga	gat	459
Thr	Gly	Ile	Ser	Ser	Ala	Val	Phe	Leu	Glu	Ser	Gly	Asn	Gly	Gly	Asp	
95		100			105											
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Val	Ser	Pro	Ala	Ala	Arg	Leu	Ala	Ala	Thr	Glu	Asn	Ala	Ser	Pro	Arg	
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gga	gga	aaa	gaa	ccg	gtg	atg	gcf	gct	aaa	gat	gag	acg	gtg	gaa	atc	555
Gly	Gly	Lys	Glu	Pro	Val	Met	Ala	Ala	Lys	Asp	Glu	Thr	Val	Glu	Ile	
125		130			135											
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Ala	Thr	Ala	Met	Glu	Ala	Ala	Glu	Leu	Ser	Gly	Tyr	Ala	Pro	Gly		
140		145			150			155								
ata	ctc	tcc	cct	tct	ccg	gct	atg	tta	ccg	aca	gct	tct	gcc	gga	ata	651
Ile	Leu	Ser	Pro	Ser	Pro	Ala	Met	Leu	Pro	Thr	Ala	Ser	Ala	Gly	Ile	
160		165			170											
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Phe	Ser	Gln	Met	Thr	His	Gln	Gly	Gly	Met	Phe	Ser	Pro	Gly	Leu		

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Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro 35 40 45			
Ala Pro Pro Pro Gln His Arg Asp Gln Ala Pro Leu Tyr Ala Ala Arg 50 55 60			
Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Thr Thr 65 70 75 80			
Ala Ser Asp Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser 85 90 95			
Ala Val Phe Leu Glu Ser Gly Asn Gly Gly Asp Val Ser Pro Ala Ala 100 105 110			
Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro 115 120 125			
Val Met Ala Ala Lys Asp Glu Thr Val Glu Ile Ala Thr Ala Met Glu 130 135 140			
Glu Ala Ala Glu Leu Ser Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser 145 150 155 160			

Pro Ala Met Leu Pro Thr Ala Ser Ala Gly Ile Phe Ser Gln Met Thr
165 170 175

Thr His Gln Gly Gly Met Phe Ser Pro Gly Leu Phe Ser Pro Ala Gly
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